RESULT 1
HUMDAF

LOCUS	HUMDAF 2017 bp mRNA linear PRI 02-NOV-1994
DEFINITION	Human complement decay-accelerating factor (DAF) mRNA; 3' end.
ACCESSION	M15799
VERSION	M15799.1 GI:181462
KEYWORDS	complement decay-accelerating factor.
SOURCE	Human HeLa cell cDNA to mRNA, clones DF1 and DF2.
ORGANISM	Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
REFERENCE	1 (bases 1 to 2017)
AUTHORS	Medof,M E , Lublin,D M , Holers,V M , Ayers,D J , Getty,R R , Leykam,J F , Atkinson,J P and Tykocinski,M L
TITLE	Cloning and characterization of cDNAs encoding the complete

```
            sequence of decay-accelerating factor of human complement
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (7), 2007-2011 (1987)
  MEDLINE   87175602
   PUBMED   2436222
 COMMENT    Draft entry and computer-readable sequence [1] kindly provided by
            M.L.Tykocinski, 24-OCT-1988.
FEATURES             Location/Qualifiers
     source          1. .2017
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="1q32"
     gene            1. .2017
                     /gene="DAF"
     mRNA            <1. .2017
                     /gene="DAF"
                     /product="DAF mRNA"
     CDS             <1. .1131
                     /gene="DAF"
                     /note="decay-accelerating factor precursor"
                     /codon_start=1
                     /protein_id="AAA52167.1"
                     /db_xref="GI:181463"
                     /db_xref="GDB:G00-119-088"
                     /translation="PSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPAL
                     EGRTSFPEDTVITYKCEESFVKIPGEKDSVTCLKGMQWSDIEEFCNRSCEVPTRLNSA
                     SLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPN
                     PGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREI
                     YCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPP
                     ECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKH
                     FHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
     sig_peptide     <1. .87
                     /gene="DAF"
                     /note="decay-accelerating factor signal peptide"
     mat_peptide     88. .1128
                     /gene="DAF"
                     /product="decay-accelerating factor"
BASE COUNT      654 a    390 c    414 g    559 t
ORIGIN      186 bp upstream of HindIII site.

  Query Match           100.0%;  Score 2017;  DB 9;  Length 2017;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 60

Qy      61 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 120

Qy     121 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 180

Qy     181 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTAAGGGCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTAAGGGCATG 240

Qy     241 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 300

Qy     301 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 360

Qy     361 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 420

Qy     421 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 480

Qy     481 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 540

Qy     541 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 600

Qy     601 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 660

Qy     661 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 720

Qy     721 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 780

Qy     781 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 840

Qy     841 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 900

Qy     901 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 960

Qy     961 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1020

Qy    1021 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1080

Qy    1081 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1140

Qy    1141 AGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1200

Qy    1201 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1260

Qy    1261 ATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 ATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTA 1320

Qy    1321 GCACACCTGCGCCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCCTTTCCTA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GCACACCTGCGCCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCCTTTCCTA 1380

Qy    1381 AAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTAAGAATGGGATCACGAGGAAAAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTAAGAATGGGATCACGAGGAAAAGAGA 1440

Qy    1441 AGGAAAGTGATTTTTTTCCACAAGATCTGAAATGATATTTCCACTTATAAAGGAAATAAA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 AGGAAAGTGATTTTTTTCCACAAGATCTGAAATGATATTTCCACTTATAAAGGAAATAAA 1500

Qy    1501 AAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAA 1560
```

```
Qy    1561 GCAAAATTGCTAAAGAGAGATGACCACATTATAAAGTAATCTTTGGCTAAGGCATTTTCA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCAAAATTGCTAAAGAGAGATGACCACATTATAAAGTAATCTTTGGCTAAGGCATTTTCA 1620

Qy    1621 TCTTTCCTTCGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGTGTTG 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCTTTCCTTCGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGTGTTG 1680

Qy    1681 ATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGA 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGA 1740

Qy    1741 GTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGA 1800

Qy    1801 GATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATA 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATA 1860

Qy    1861 GTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATTTATGACAGTGAA 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 GTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATTTATGACAGTGAA 1920

Qy    1921 CATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTAT 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTAT 1980

Qy    1981 TTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2017
           |||||||||||||||||||||||||||||||||||
Db    1981 TTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2017
```

ALIGNMENTS

RESULT 1
HUMDAFA
LOCUS HUMDAFA 2220 bp mRNA linear PRI 02-NOV-1994
DEFINITION Human decay-accelerating factor mRNA, complete cds.
ACCESSION M30142
VERSION M30142.1 GI:181464
KEYWORDS Alu repeat; alternative splicing; decay-accelerating factor; membrane glycoprotein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Caras,I.W., Davitz,M.A., Rhee,L., Weddell,G., Martin,D.W. Jr. and Nussenzweig,V.

```
TITLE     Cloning of decay-accelerating factor suggests novel use of splicing
          to generate two proteins
JOURNAL   Nature 325 (6104), 545-549 (1987)
MEDLINE   87115845
 PUBMED   2433596
COMMENT   The gene for decay accelerating factor produces two proteins by
          alternative splicing.  The spliced out region is from position
          1147-1265.  The stop codon in this case is located at position
          1327-1329.  Though mRNAs do not have introns, the alternative
          coding region is indicated in the features table.
FEATURES             Location/Qualifiers
     source          1. .2220
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="1q32"
                     /cell_line="HeLa"
     mRNA            <1. .2220
                     /gene="DAF"
                     /note="G00-119-088"
     gene            join(66. .1146,1265. .1329)
                     /gene="DAF"
     CDS             join(66. .1146,1265. .1329)
                     /gene="DAF"
                     /codon_start=1
                     /product="decay-accelerating factor A"
                     /protein_id="AAA52168.1"
                     /db_xref="GI:181465"
                     /db_xref="GDB:G00-119-088"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
                     AQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPT
                     RLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKK
                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
     sig_peptide     66. .167
                     /gene="DAF"
                     /note="G00-119-088"
     mat_peptide     join(168. .1146,1265. .1326)
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     exon            <66. .1146
                     /gene="DAF"
                     /note="decay-accelerating factor precursor A"
                     /number=1
     mat_peptide     168. .1385
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     intron          1147. .1264
                     /gene="DAF"
                     /note="G00-119-088"
     repeat_region   1150. .1264
                     /note="Alu repeat (partial)"
     exon            1265. .>1329
                     /gene="DAF"
                     /note="G00-119-088"
                     /number=2
     polyA_signal    1410. .1415
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1693. .1698
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1731. .1736
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    2198. .2203
                     /gene="DAF"
                     /note="G00-119-088; putative"
                     2220
                     /gene="DAF"
                     /note="G00-119-088"
BASE COUNT       681 a    455 c    475 g    609 t
ORIGIN

  Query Match          100.0%;  Score 2220;  DB 9;  Length 2220;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2220;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
Db     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
Db     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
Db     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
Db     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
Db     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
```

```
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGGTTCTCGTCCTGTCACCCAGGCTGGTATGCGGTGGTGTGATCGTAGCTCACTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TATCTGGTTCTCGTCCTGTCACCCAGGCTGGTATGCGGTGGTGTGATCGTAGCTCACTGC 1200

Qy   1201 AGTCTCGAACTCCTGGGTTCAAGCGATCCTTCCACTTCAGCCTCCCAAGTAGCTGGTACT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCTCGAACTCCTGGGTTCAAGCGATCCTTCCACTTCAGCCTCCCAAGTAGCTGGTACT 1260

Qy   1261 ACAGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ACAGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTG 1320

Qy   1321 CTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAG 1380

Qy   1381 TTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGAT 1440

Qy   1441 GCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGT 1500

Qy   1501 CCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTG 1560

Qy   1561 AGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGG 1620

Qy   1621 GATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCC 1680

Qy   1681 ACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACC 1740

Qy   1741 CAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATC 1800

Qy   1801 TTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAAC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAAC 1860

Qy   1861 ATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 ATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAA 1920

Qy   1921 TCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACT 1980

Qy   1981 TAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATT 2040

Qy   2041 ATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTAT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2041 ATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTAT 2100

Qy   2101 TTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAG 2160

Qy   2161 AAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2220
```

399

iten

o